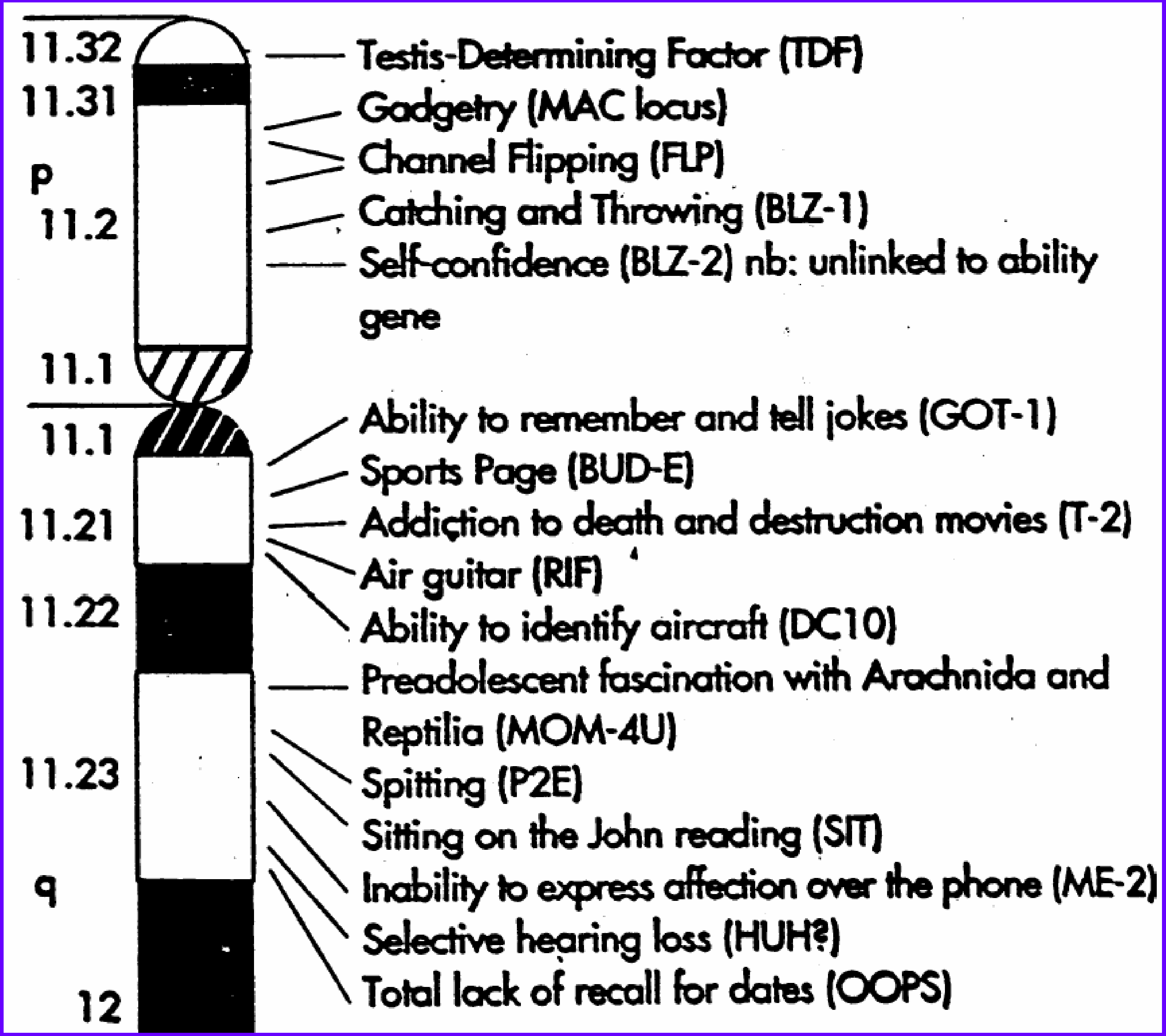
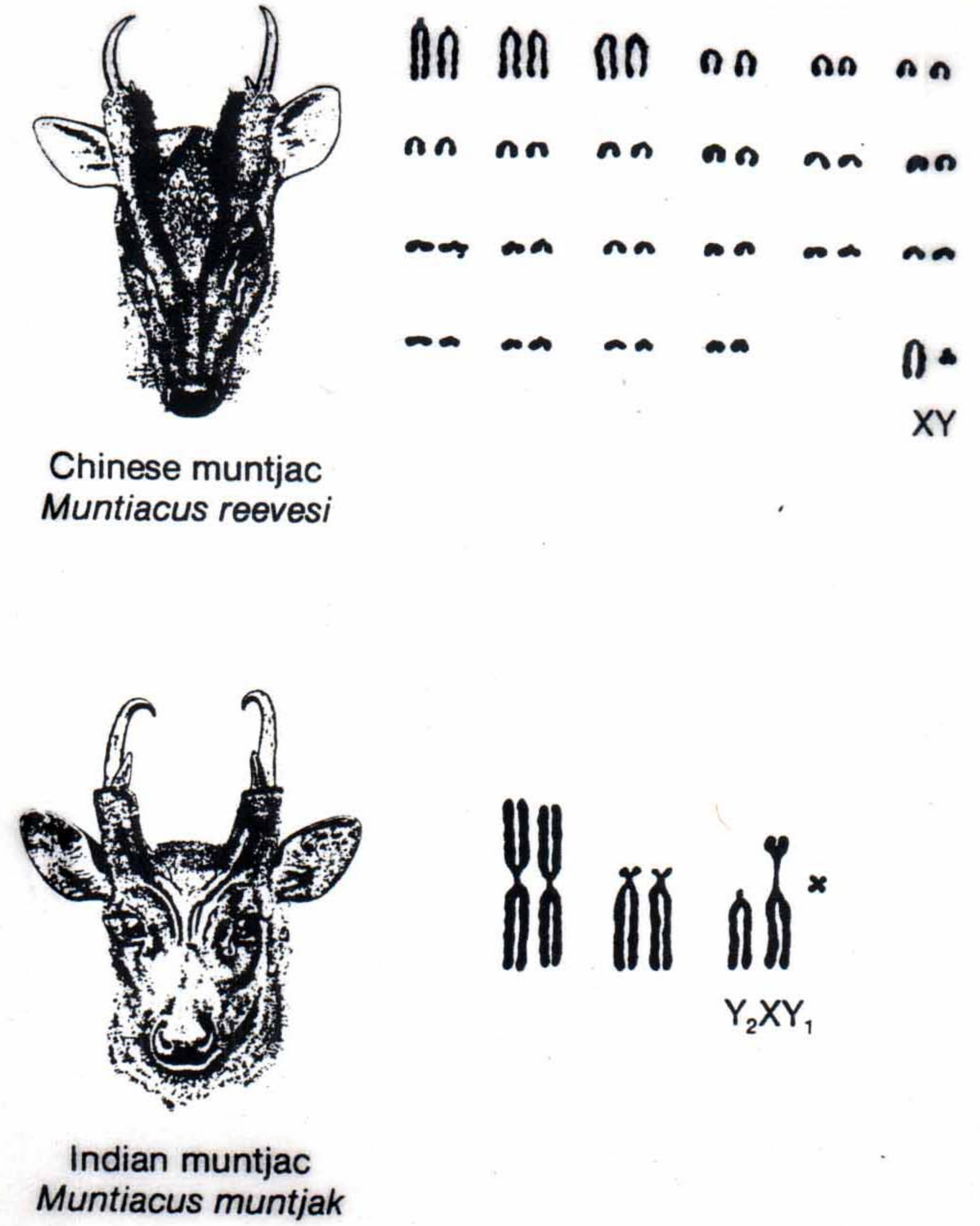
Human Y Chromosome



Chromosomal variation between species

(rearrangements, translocations)



CHROMOSOMAL VARIABILITY

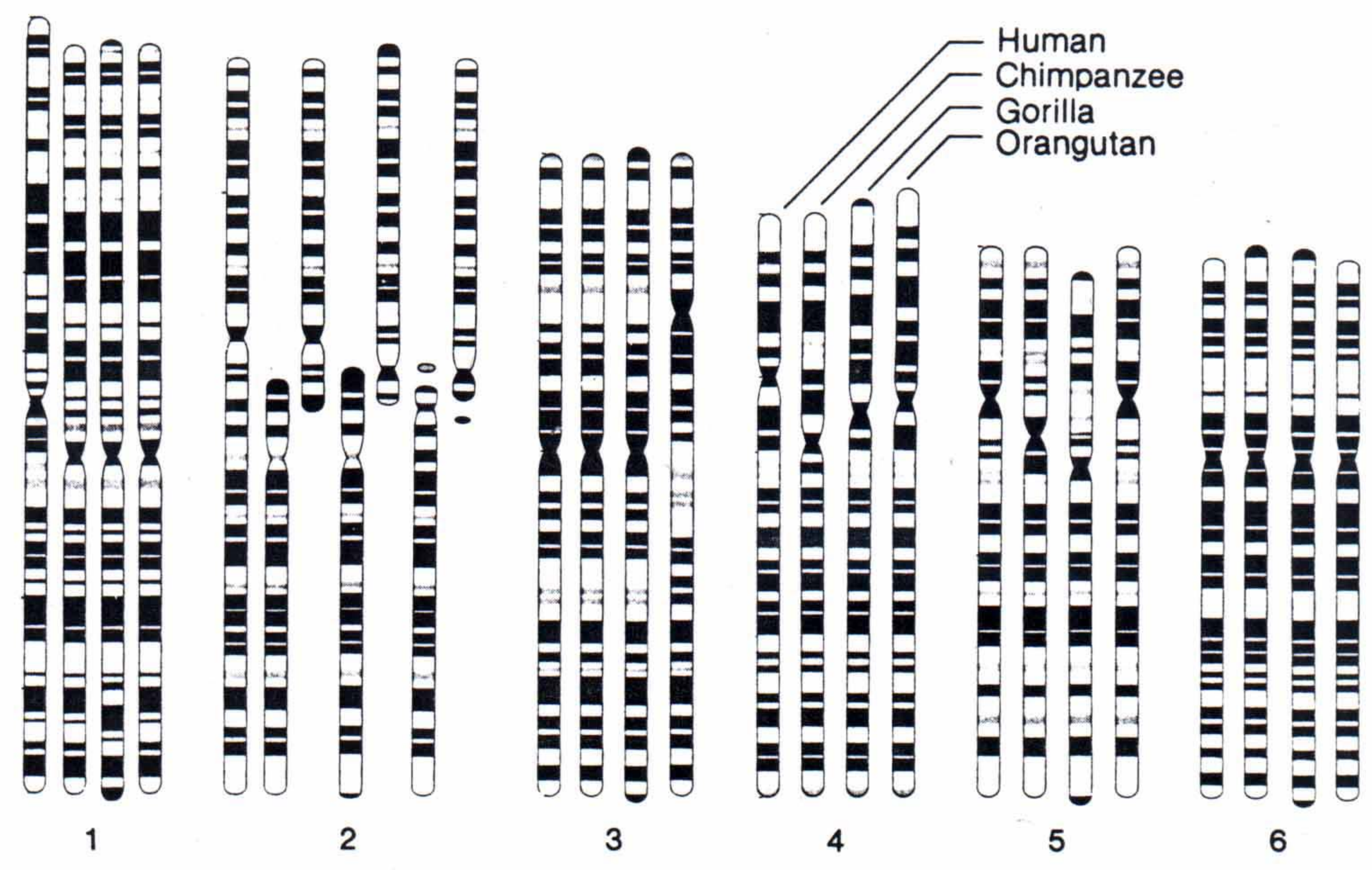
Ignored, but important for conservation:

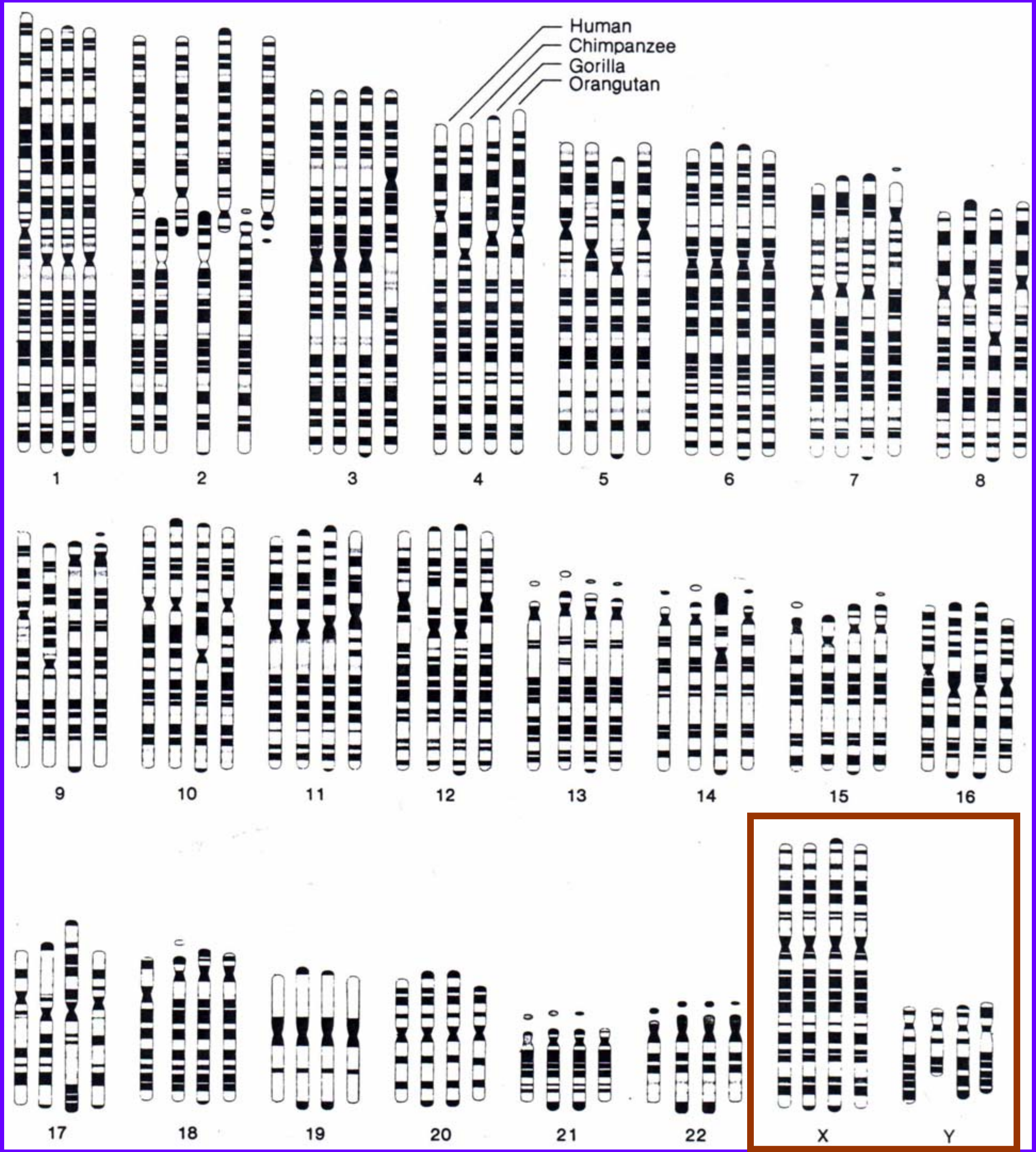
(1) Associated with reduced fertility.

(2) Taxa more likely to be threatened are also more likely to have more chromosomal variability.

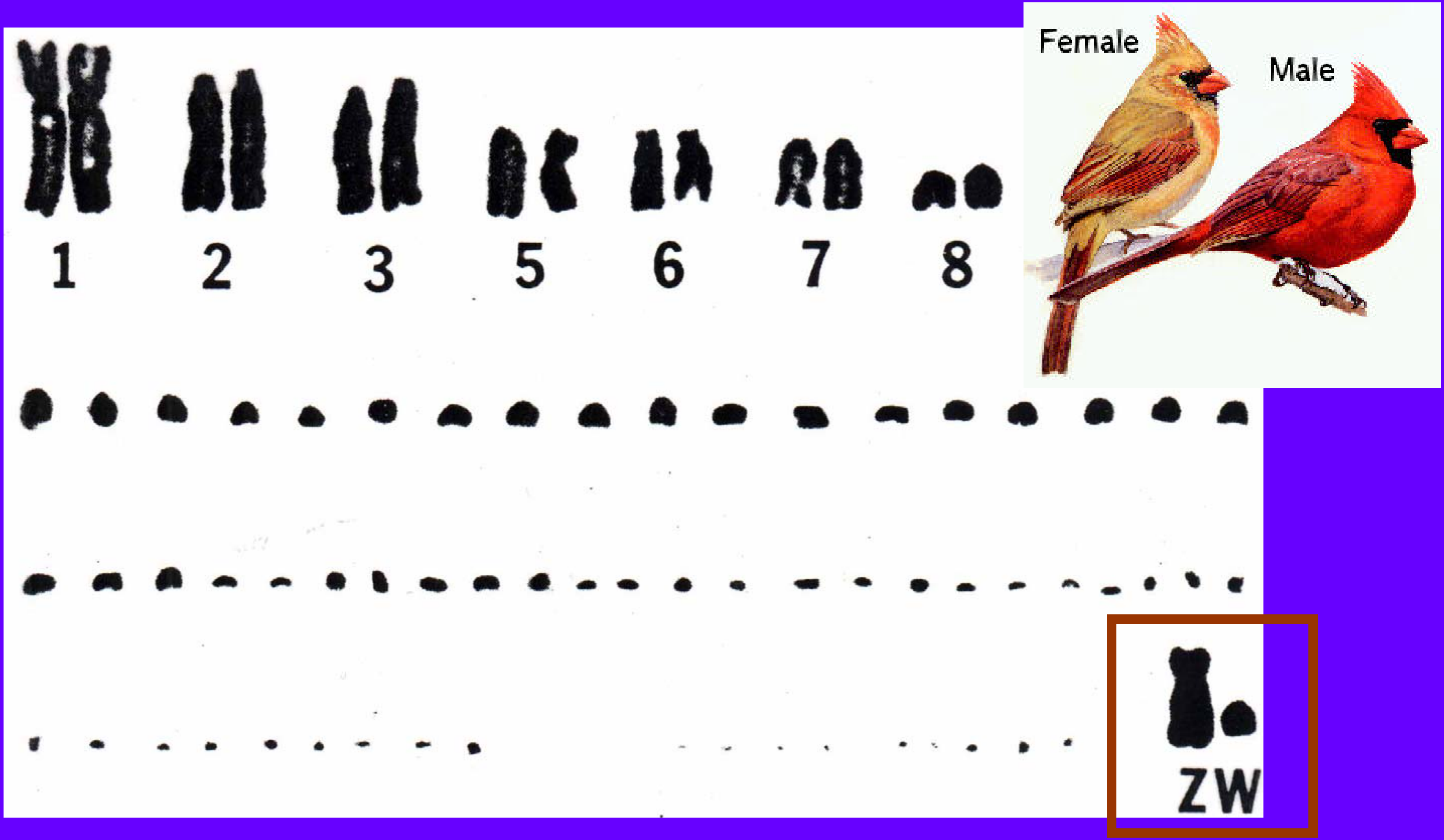
(a) Small population size

(b) Complex social structure


Human
Chimpanzee
Gorilla
Orangutan
1
2
3
4
5
6

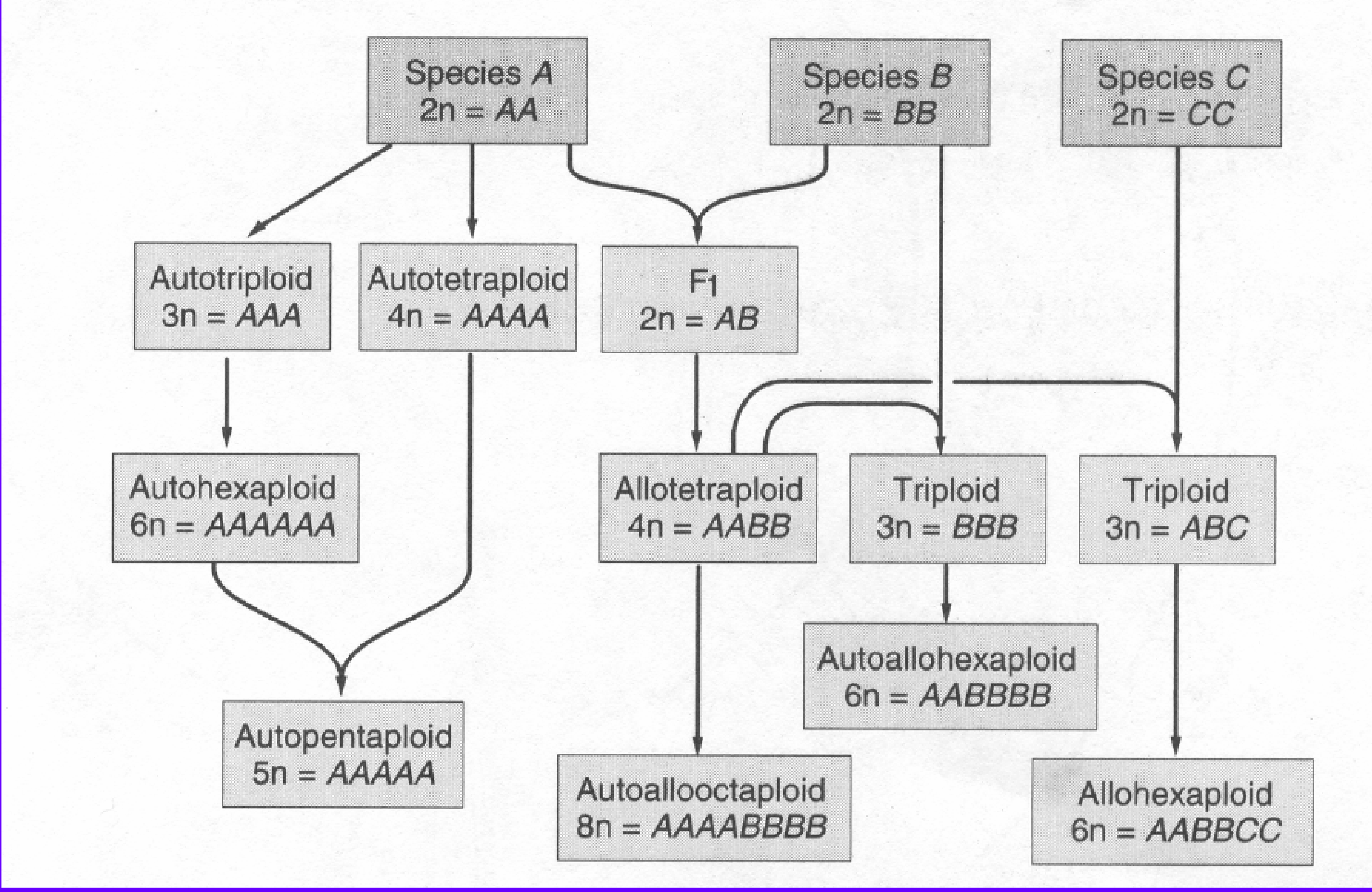


Sex Chromosomes

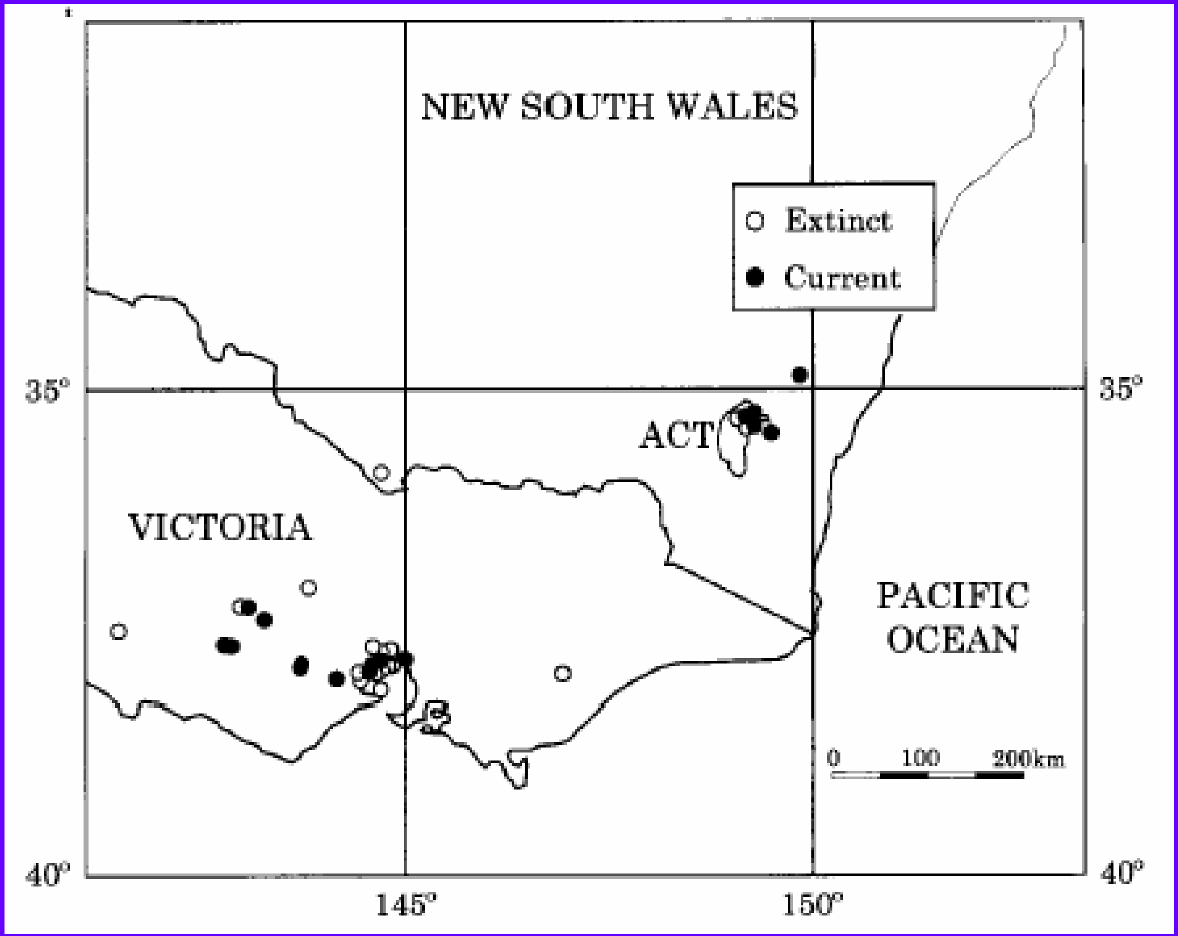


Sex Chromosomes

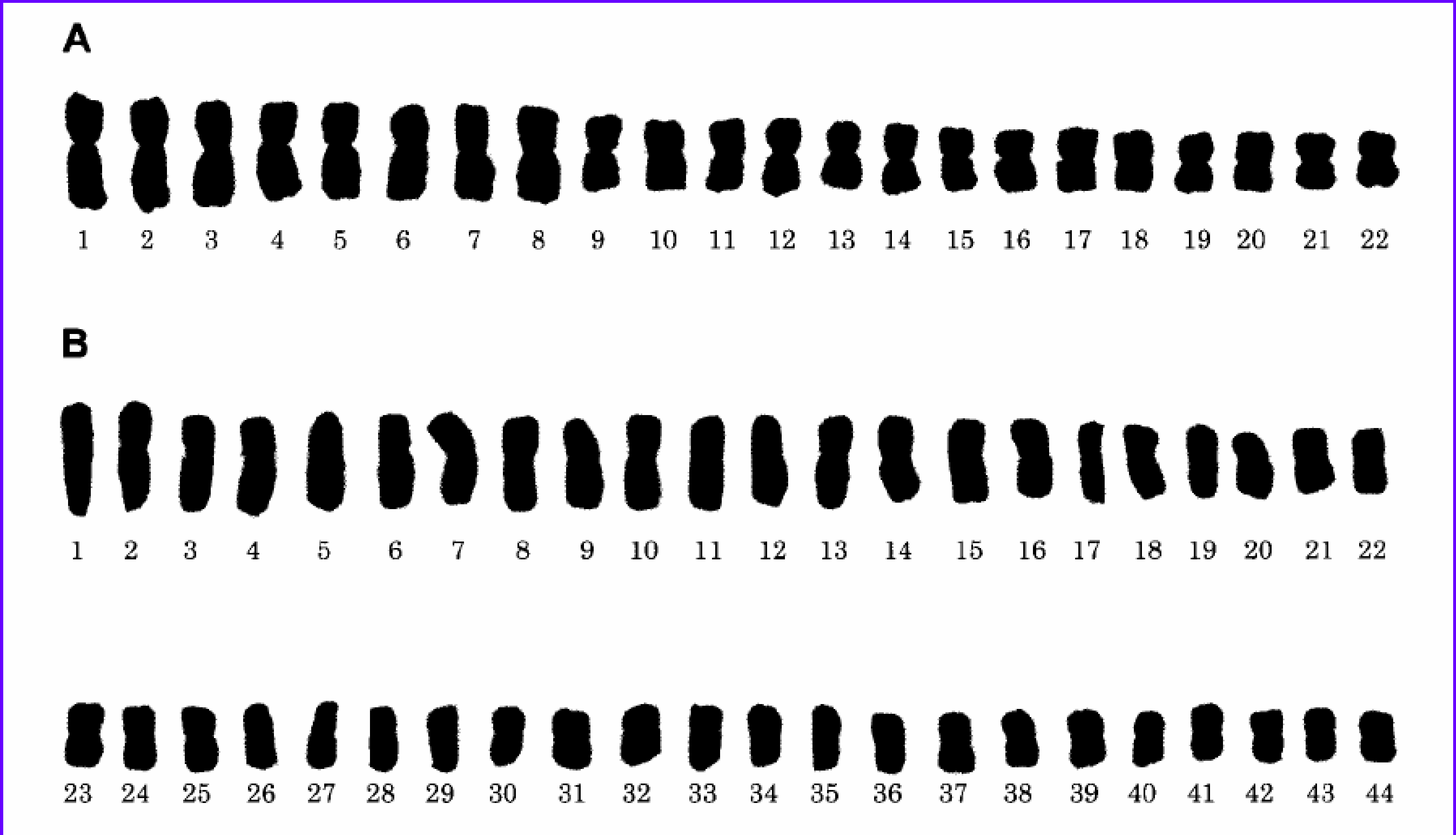
Polyploidy (n = haploid number)



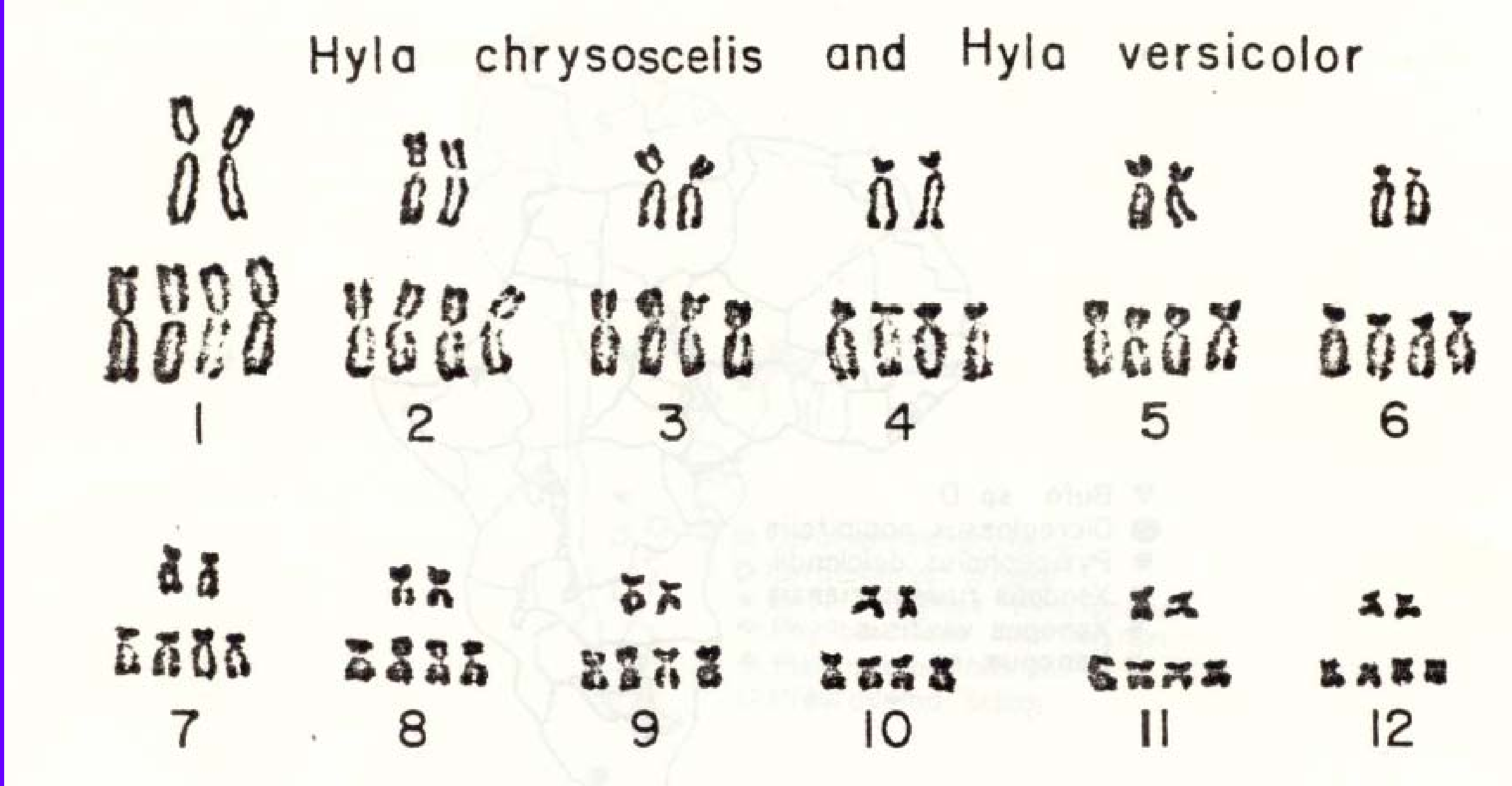
Australian grassland forb (*Rutidosis leptorrhynchoides*)



Diploid 2n=22



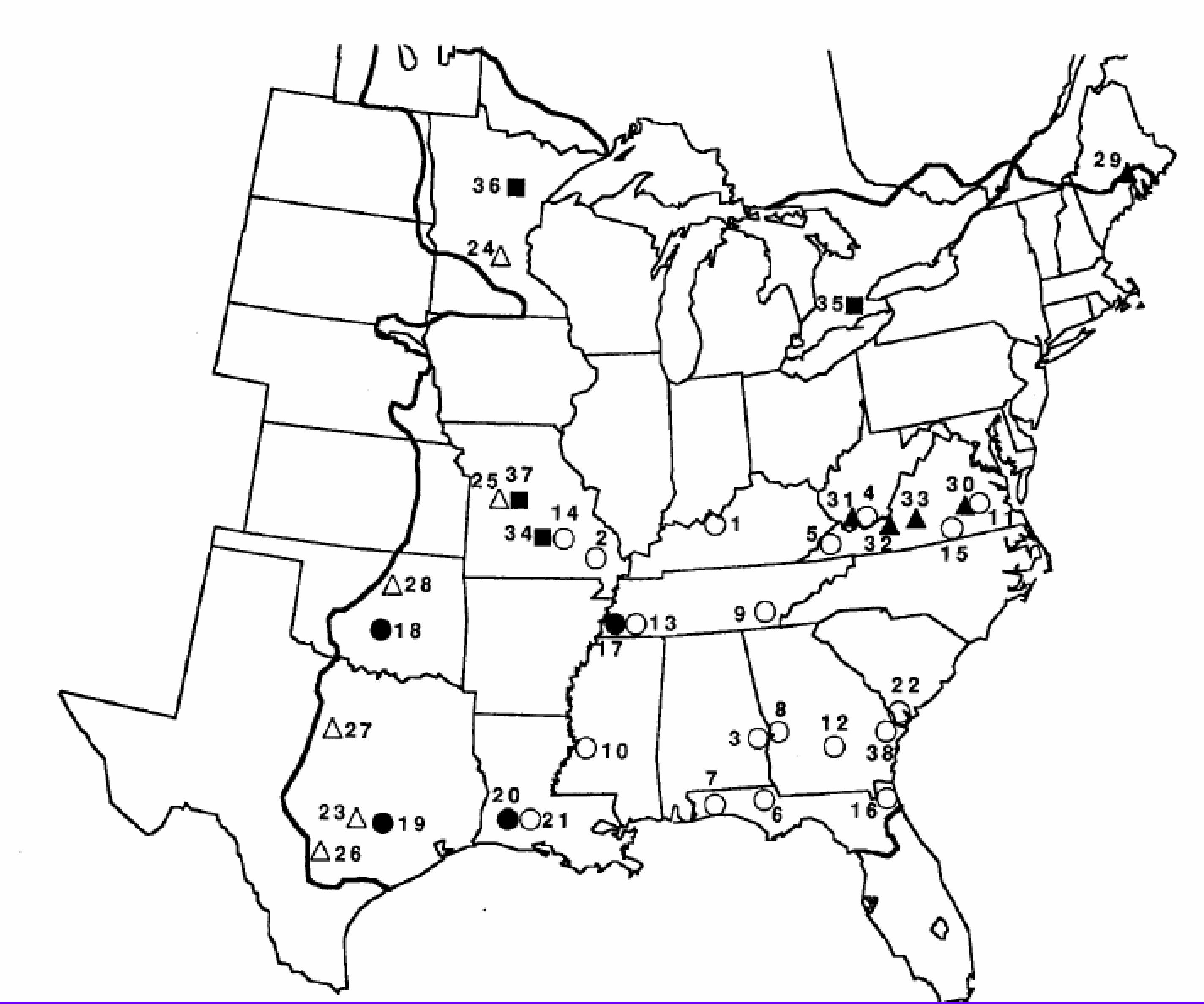
Tetraploid 4n = 44



$2n$

$4n$

$4n$ = solid shapes $2n$ = open shapes



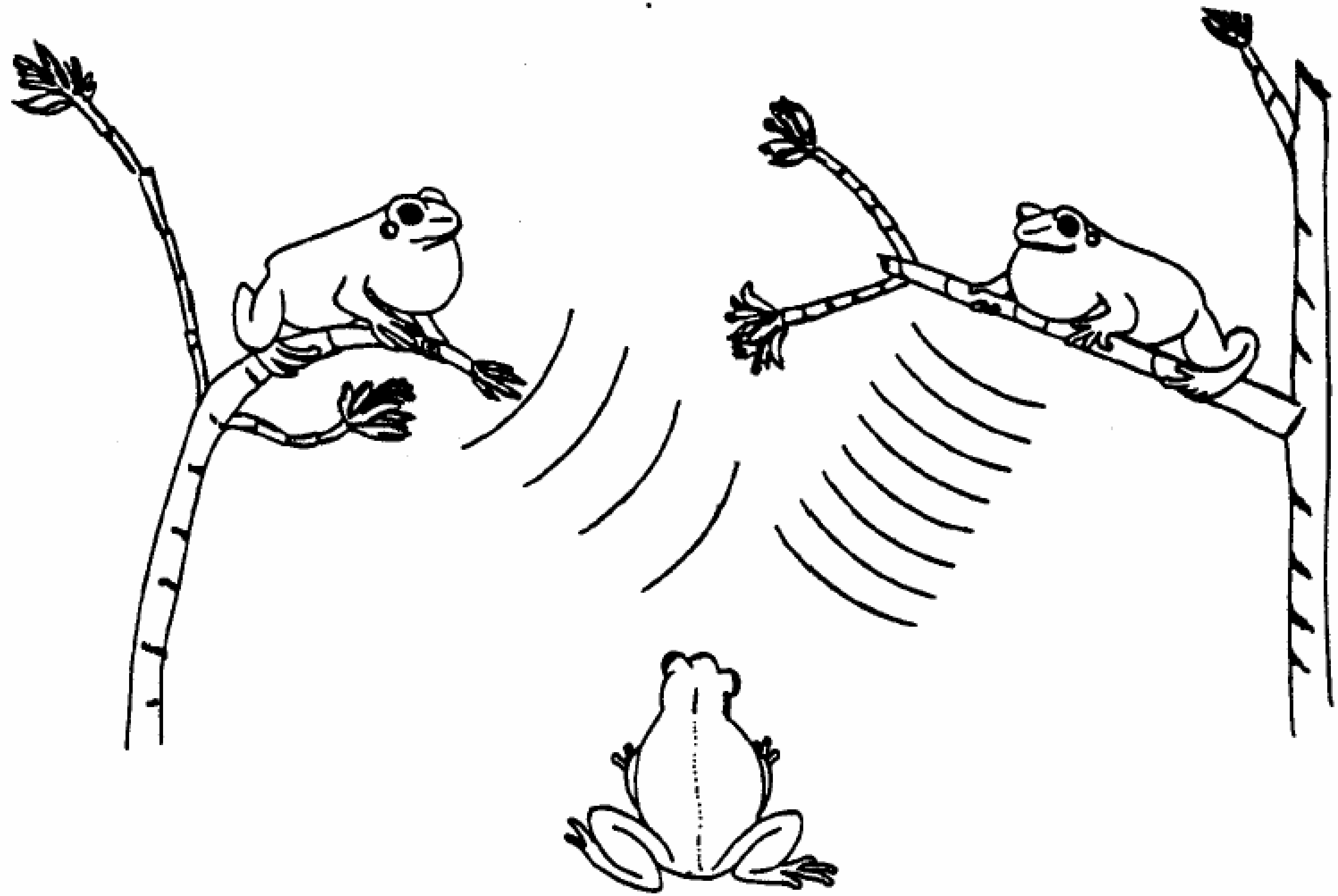
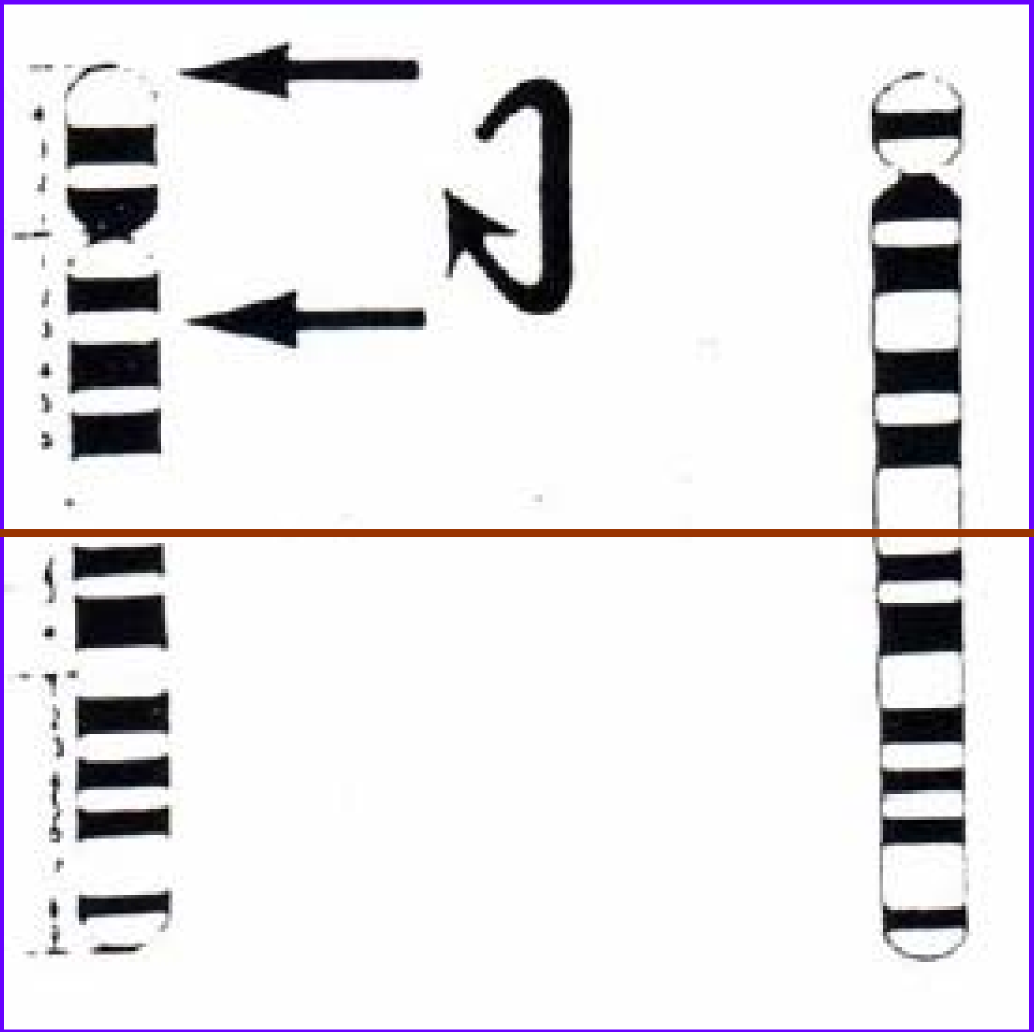


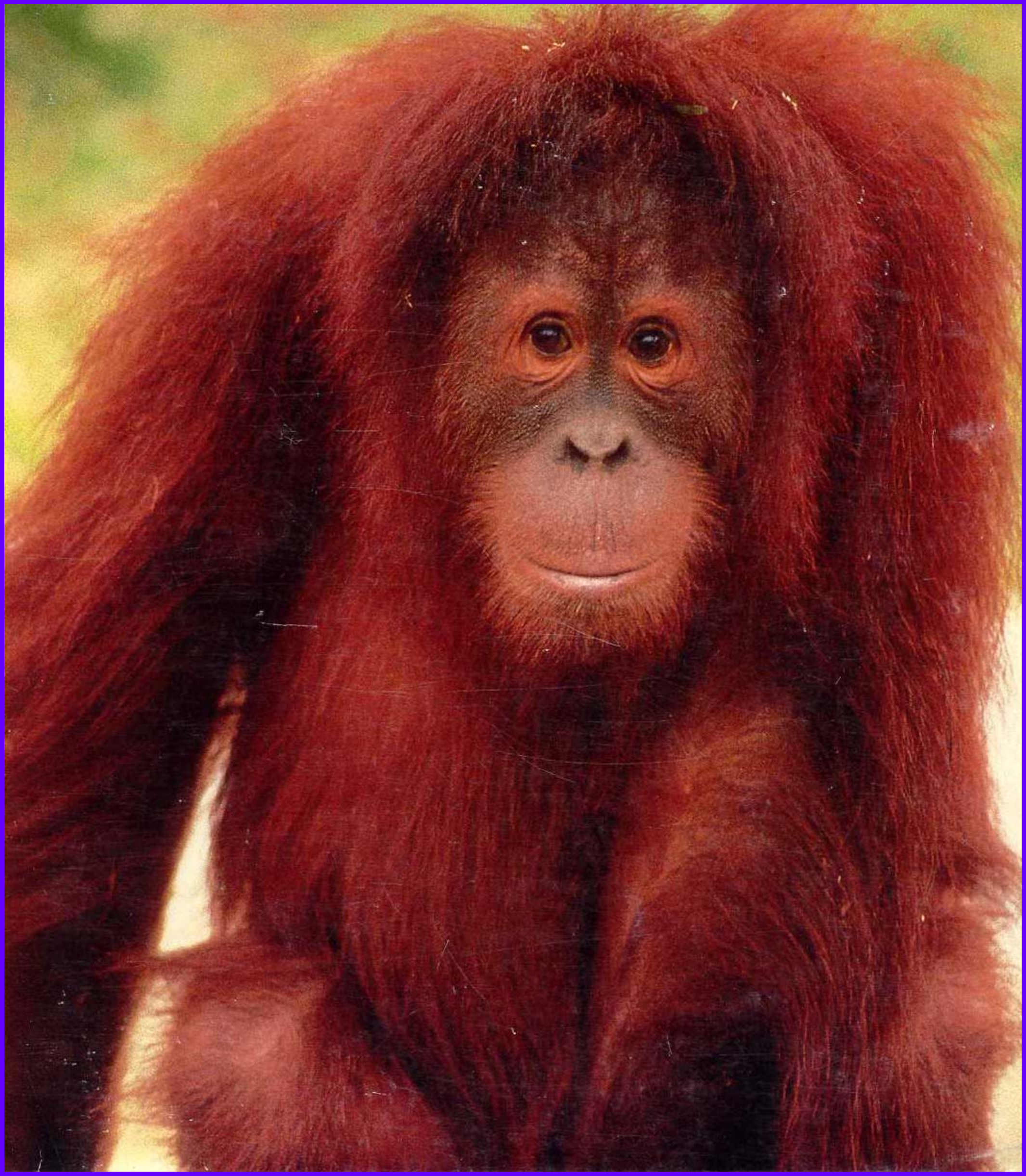
Fig. 10. Discriminating female frogs!

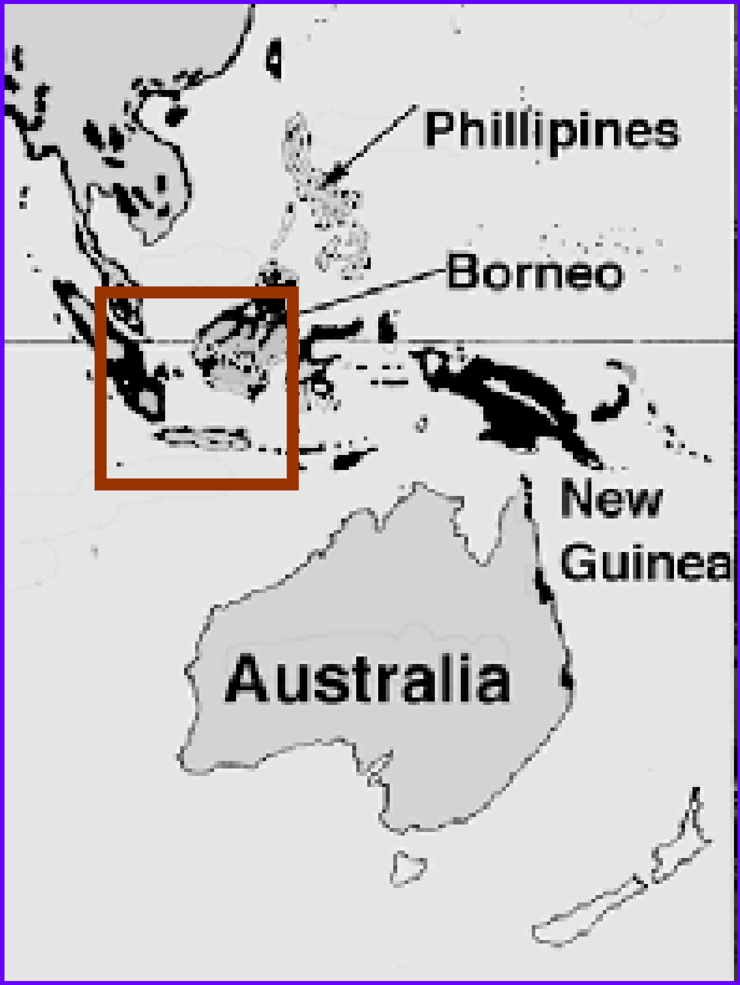
Chromosomal Inversions

Pericentric
(around)

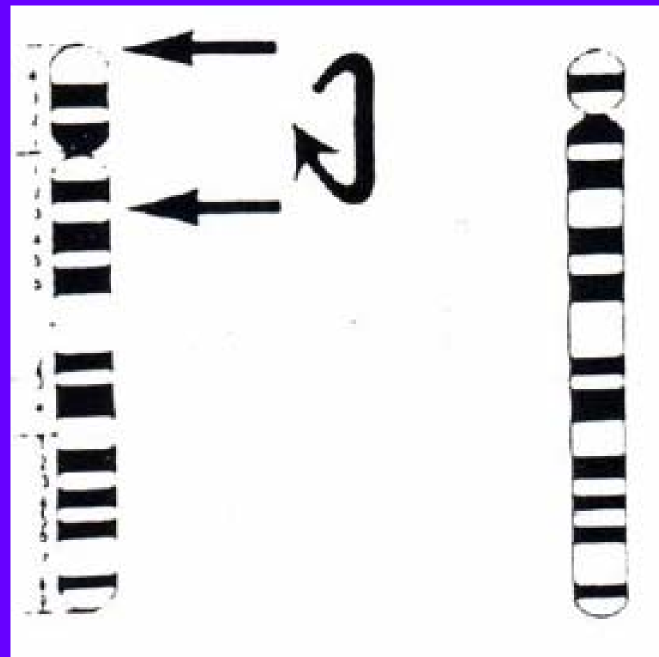
Paracentric
(beside)



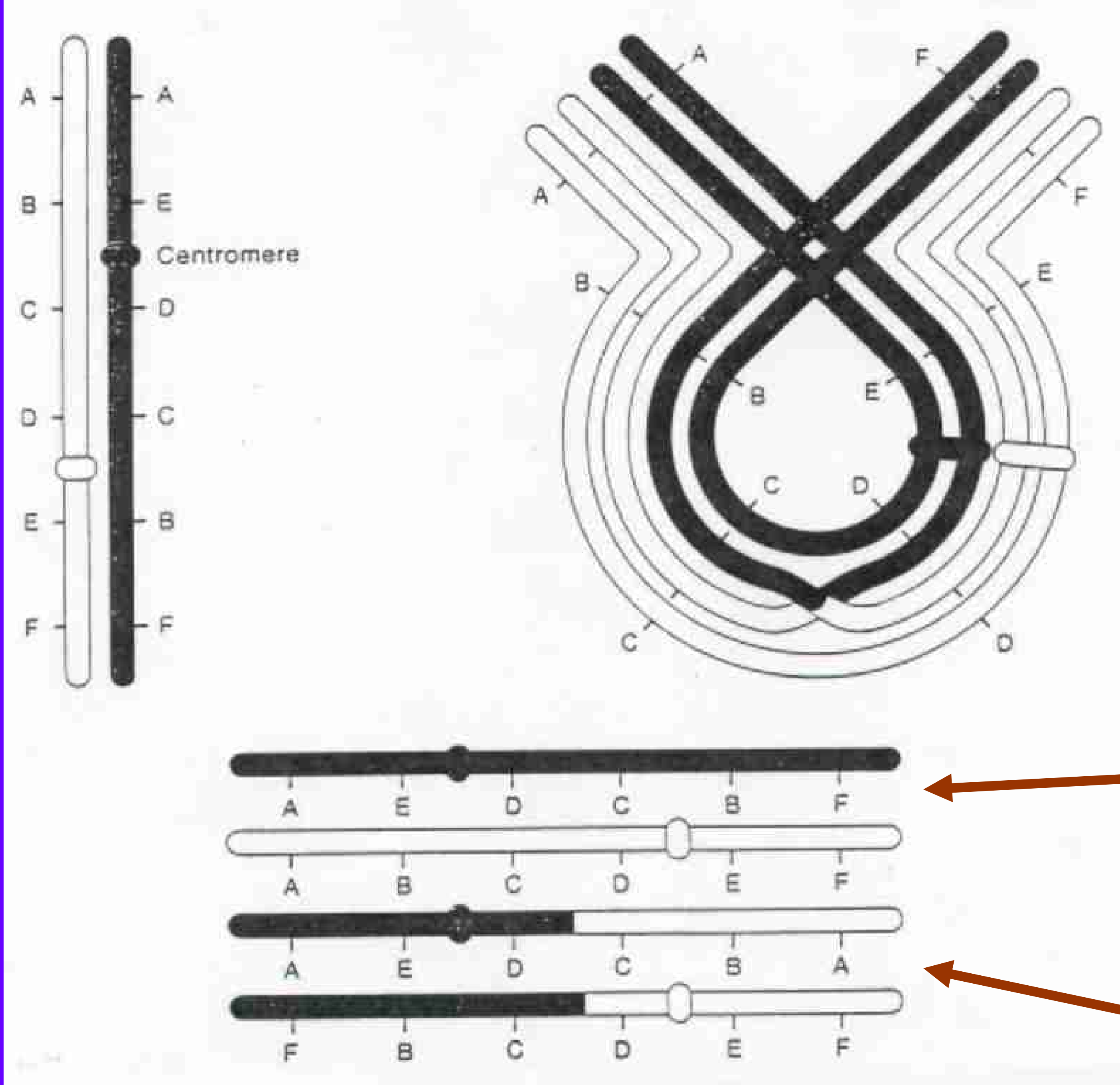



Phillipines
Borneo
New
Guinea
Australia

Sumatra



Borneo



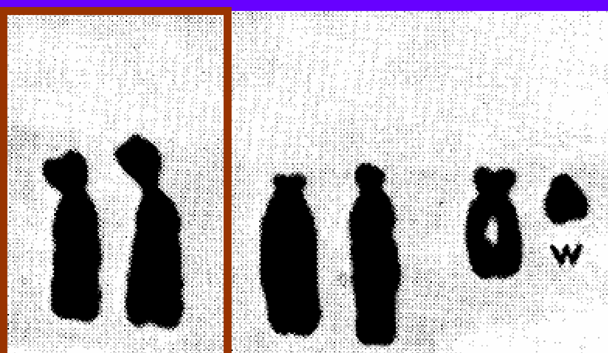
Euploid

Aneuploid

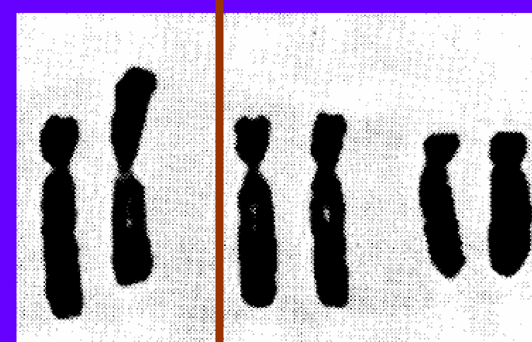
Table 3.2. Chromosomal inversion polymorphisms in the orangutan (Ryder and Chemnick 1993). The inversion in chromosome-2 distinguishes the Sumatran (*S*) and Bornean (*B*) subspecies. The two inversion types in chromosome-9 (*C* and *R*) are polymorphic in both subspecies.

	Chromosome 2			Chromosome 9		
	BB	SB	SS	CC	CR	RR
Wild born	51	0	41	67	22	3
Zoo born	90	44	82	71	34	3

White-throated sparrow



22 3^a3^a ZW



22^m 33 ZZ

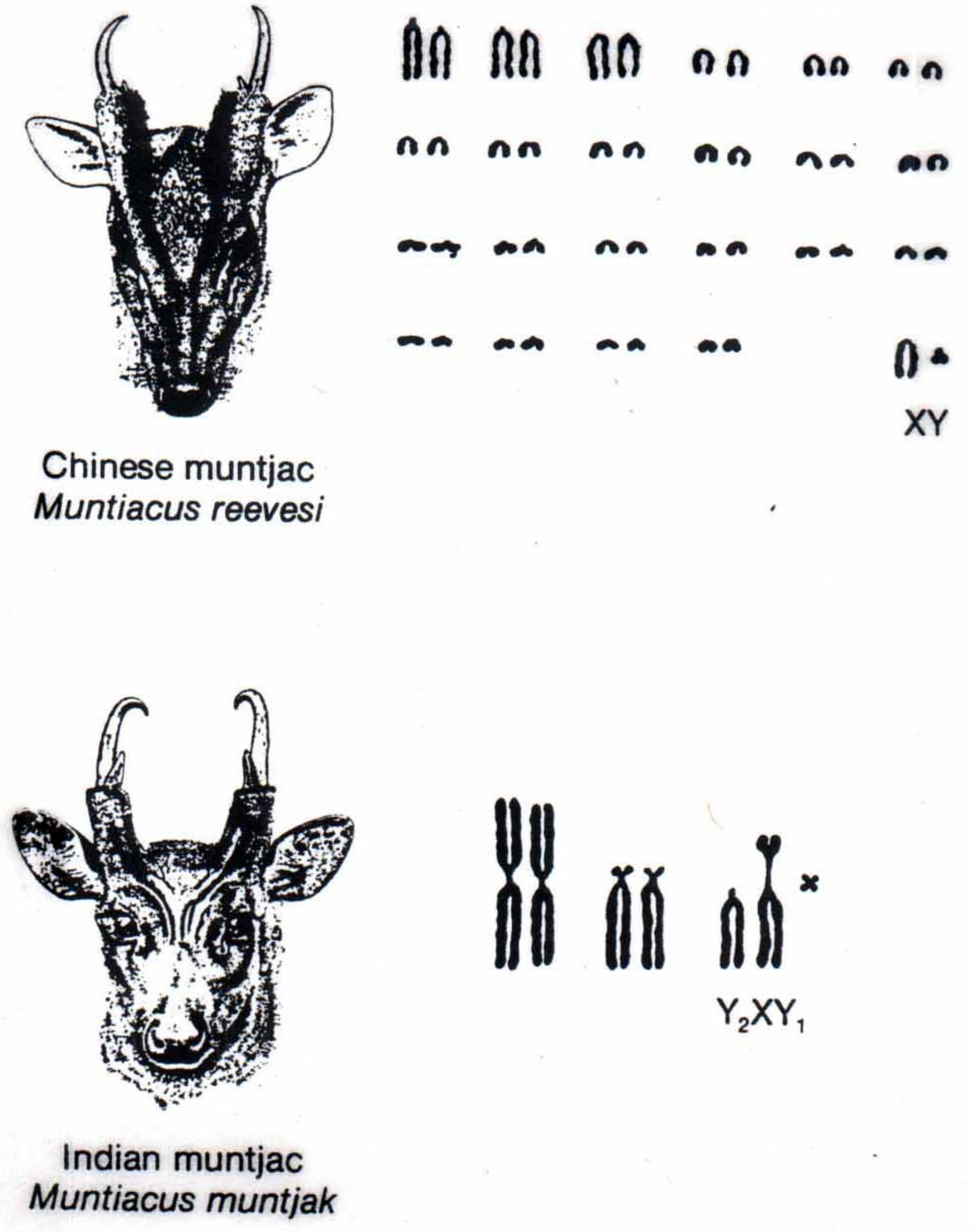
Negative assortative (disassortative) mating

TABLE 3. *Phenotypes and karyotypes of mated White-throated Sparrows.*

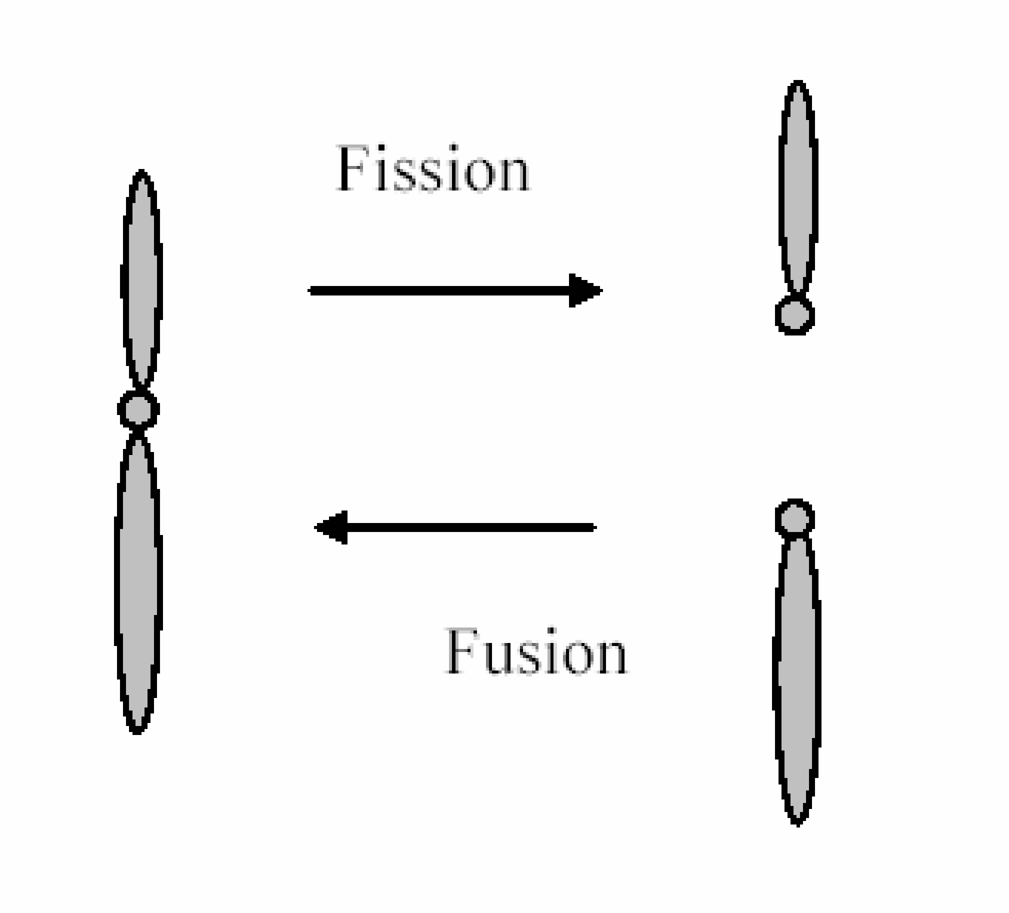
Males		Females	Observed	Expected
White-striped (22^m)	×	White-striped (22^m)	2	12.2
White-striped (22^m)	×	Tan-striped (22)	33	10.4
Tan-striped (22)	×	White-striped (22^m)	6	10.4
Tan-striped (22)	×	Tan-striped (22)	1	8.9
Totals			42	42.0

Thorneycroft, H. B. 1975. A cytogenetic study of the white-throated sparrow, *Zonotrichia albicollis* (Gmelin). Evolution 29:611-621.

Chromosomal translocations



Robertsonian Translocation



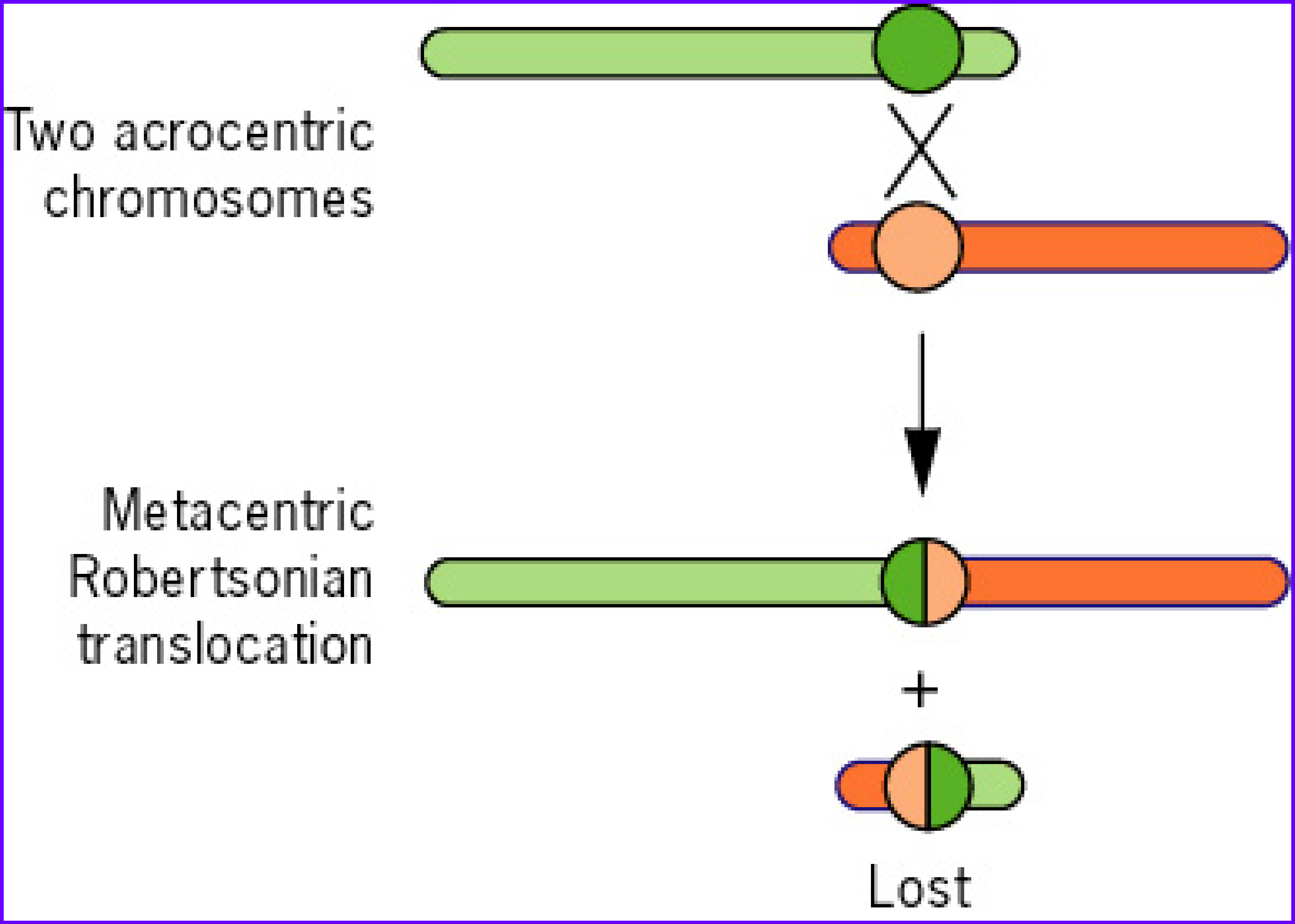
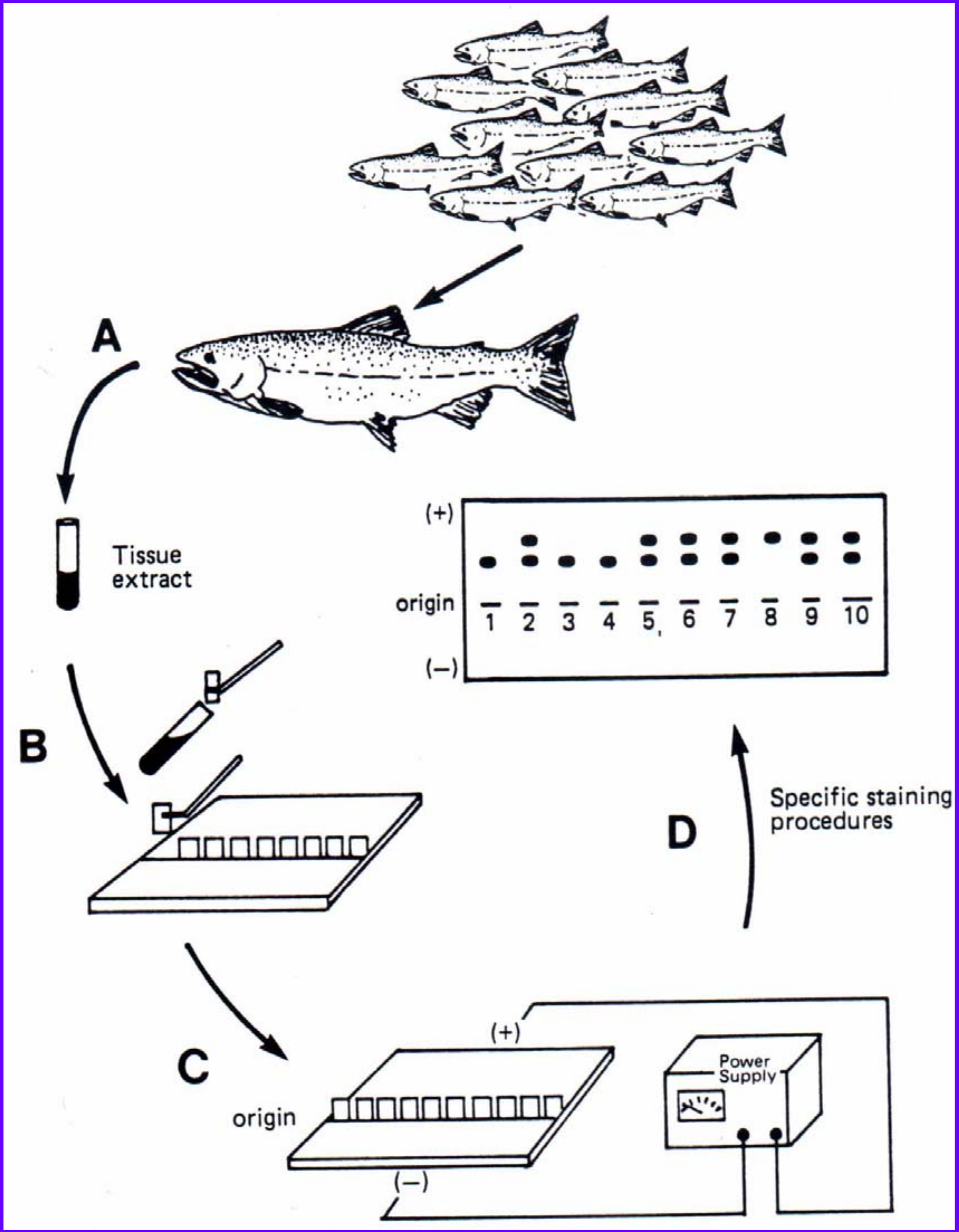

Two acrocentric chromosomes
Metacentric Robertsonian translocation
+
Lost

Table 3.3. Litter sizes produced by mice heterozygous for Robertsonian translocations characteristic of three different chromosomal races (AA, POS, and UV). From Hauffe and Searle (1998).

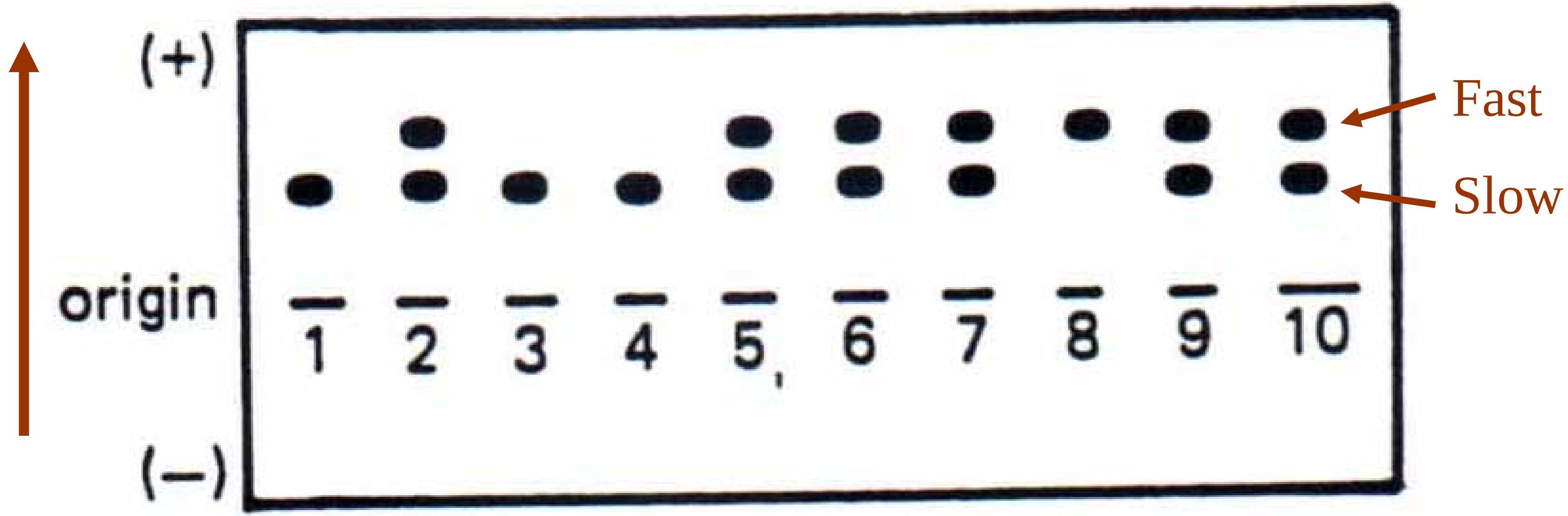
Female	Male	No. litters	Litter size
AA	AA (control)	17	6.7 ± 0.8
AA	(AA x POS)	16	4.1 ± 0.4
AA	(AA x UV)	18	2.6 ± 0.3
AA	(UV x POS)	19	3.8 ± 0.3
AA (control)	AA	18	6.8 ± 0.4
(AA x POS)	AA	7	1.0 ± 0
(AA x UV)	AA	10	3.1 ± 0.6
(POS x UV)	AA	11	4.0 ± 0.5

Protein Electrophoresis (Allozymes)

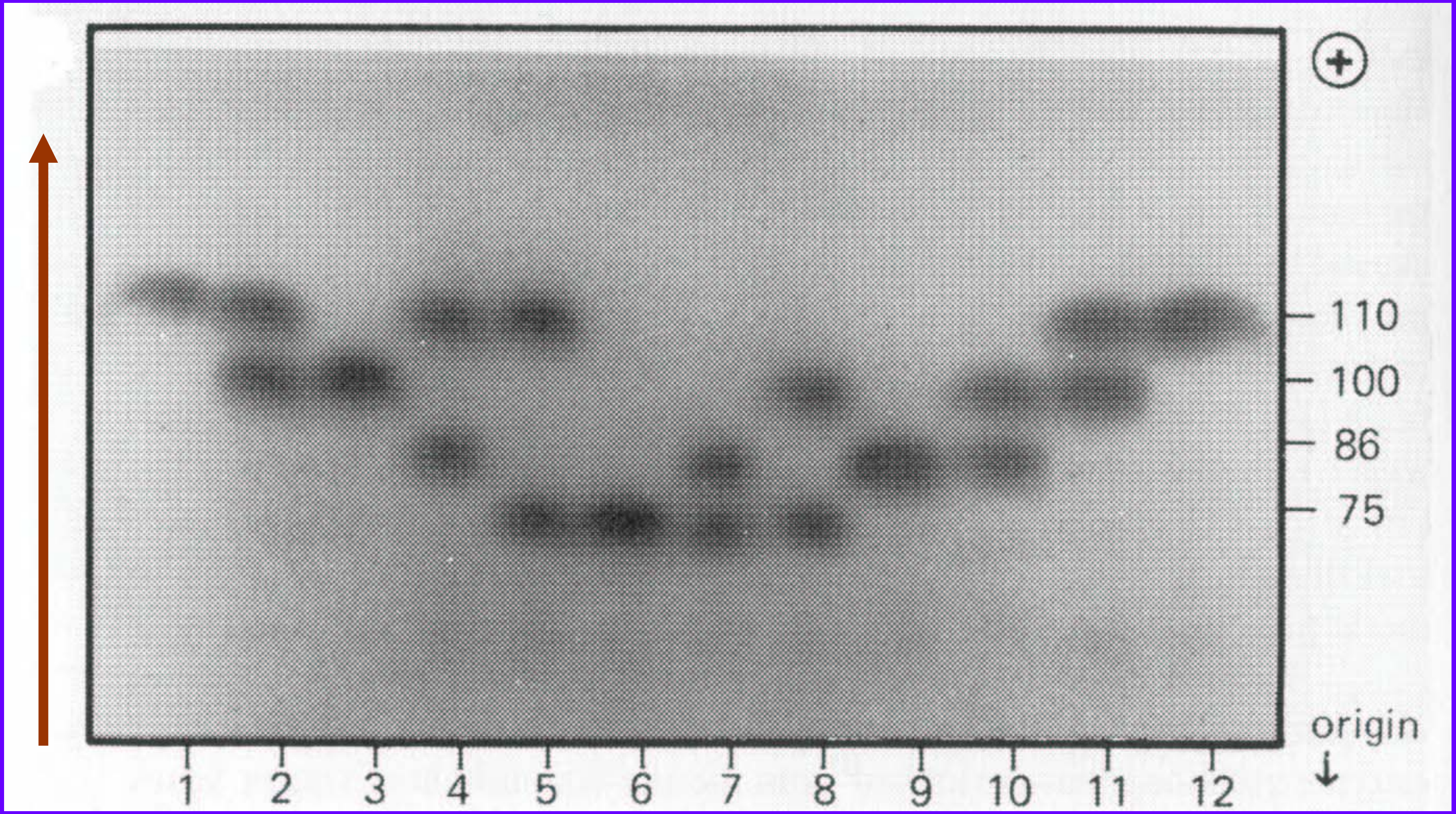
Time Period	Primary techniques
1900-1970	Laboratory matings and chromosomes
1970s	Protein electrophoresis (allozymes)
1980s	Mitochondrial DNA
1990s	Nuclear DNA
2000s	Genomics



A
Tissue extract
B
C
D
(+)
origin
1 2 3 4 5 6 7 8 9 10
(−)
Specific staining procedures
(+)
origin
(−)
Power Supply


(+)
origin
(–)
1
2
3
4
5
6
7
8
9
10
Fast
Slow

Aconitate dehydratase



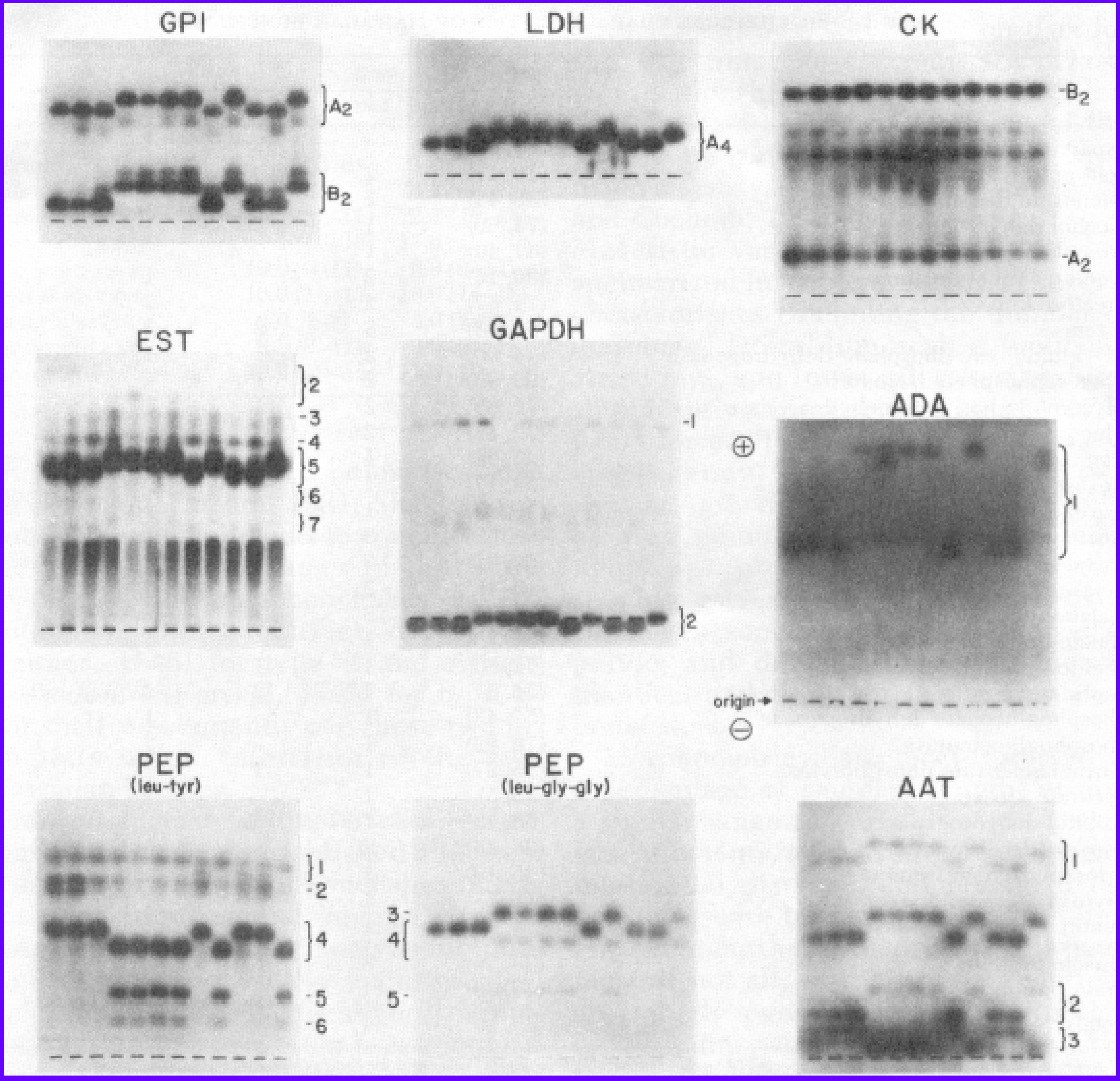
Chinook salmon

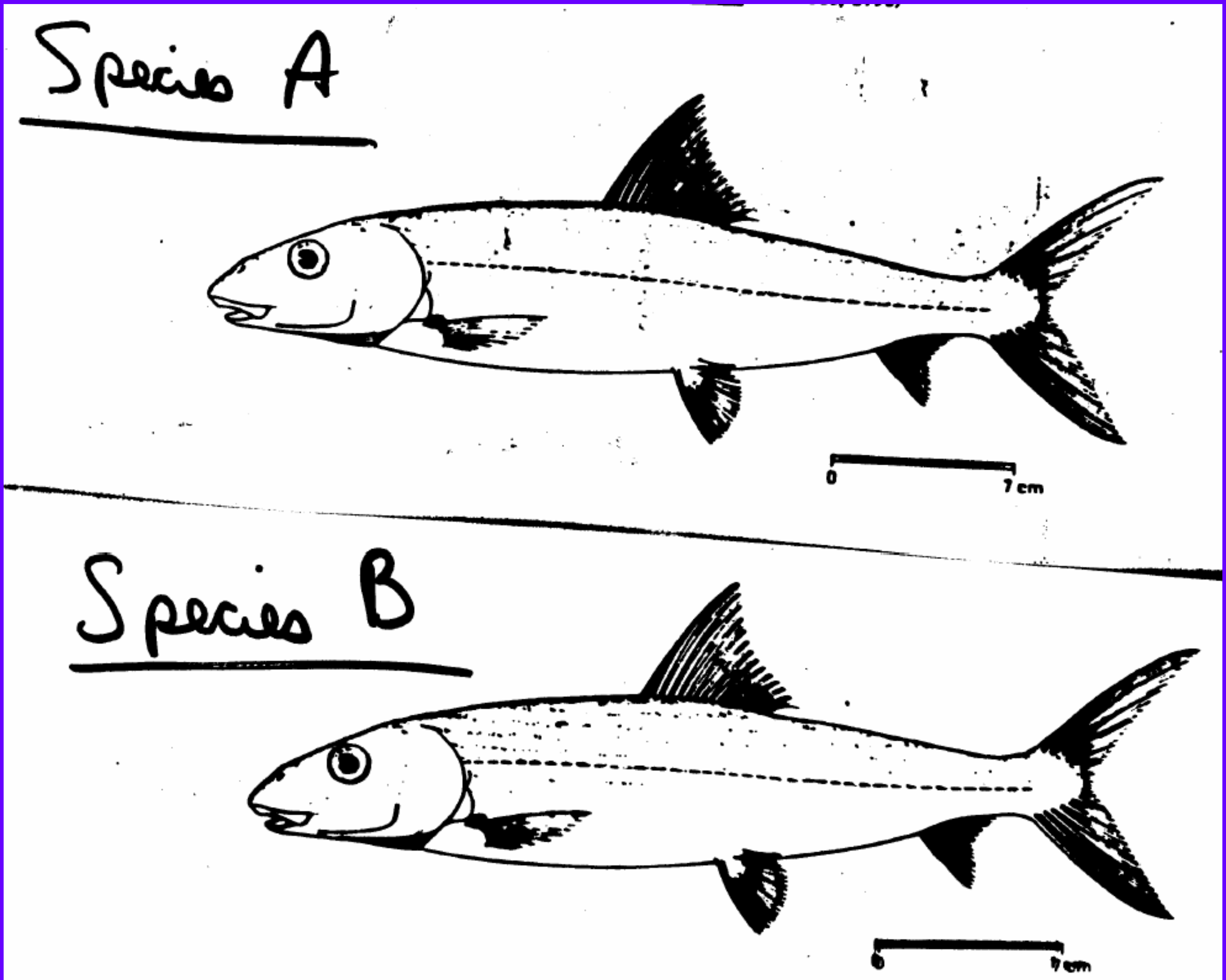
Are allozymes obsolete?

Imagine for sake of argument that DNA sequencing methods had been widely employed for the past thirty years, and that only recently had protein electophoretic approaches been introduced. No doubt a headlong rush into allozyme techniques would ensue, on justifiable grounds that: (a) the methods are cost effective and technically simple; (b) the molecular variants represent independent Mendelian polymorphisms at numerous loci scattered around the genome (rather than tightly linked variants in a single sequenced region of DNA); and (c) the amino acid replacement substitutions revealed in the protein assays might bring molecular evolutionists closer to the real "stuff" of adaptive evolution.

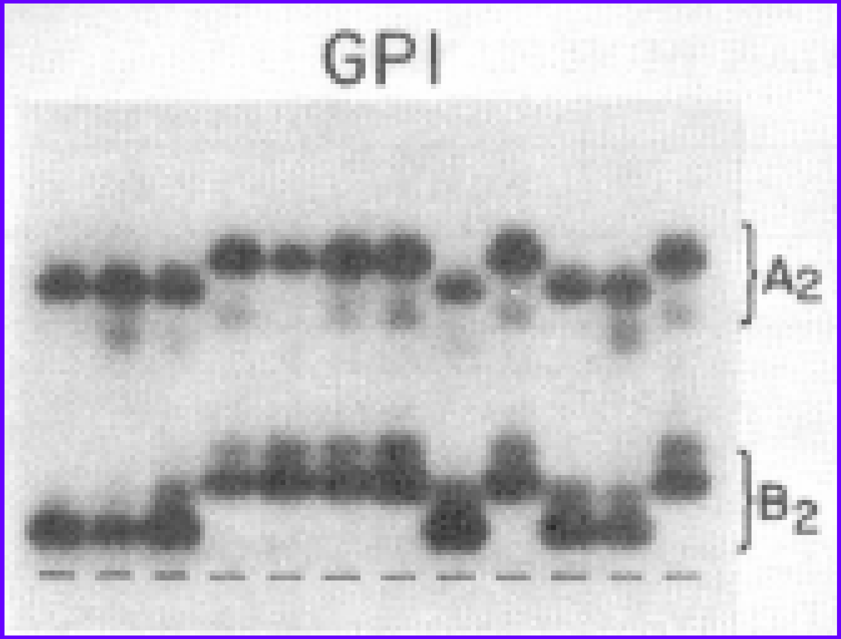
John Avise (1994)

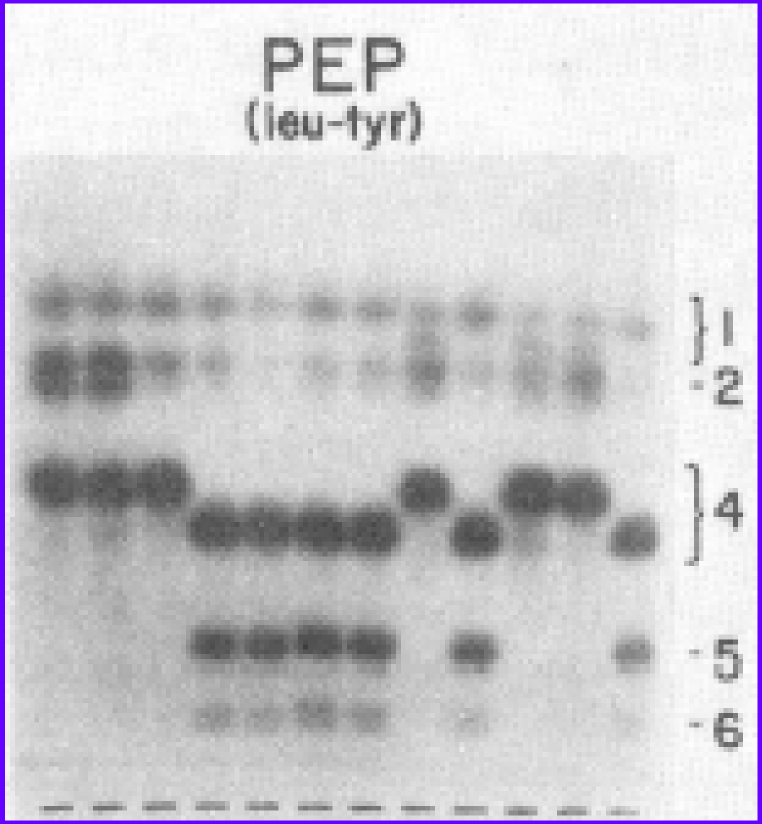
Bonefish (Shaklee and Tamaru 1981)


GPI
A2
B2
LDH
A4
CK
B2
A2
EST
2
3
4
5
6
7
GAPDH
1
2
ADA
1
origin
PEP
(leu-tyr)
1
2
4
5
6
PEP
(leu-gly-gly)
3
4
5
AAT
1
2
3

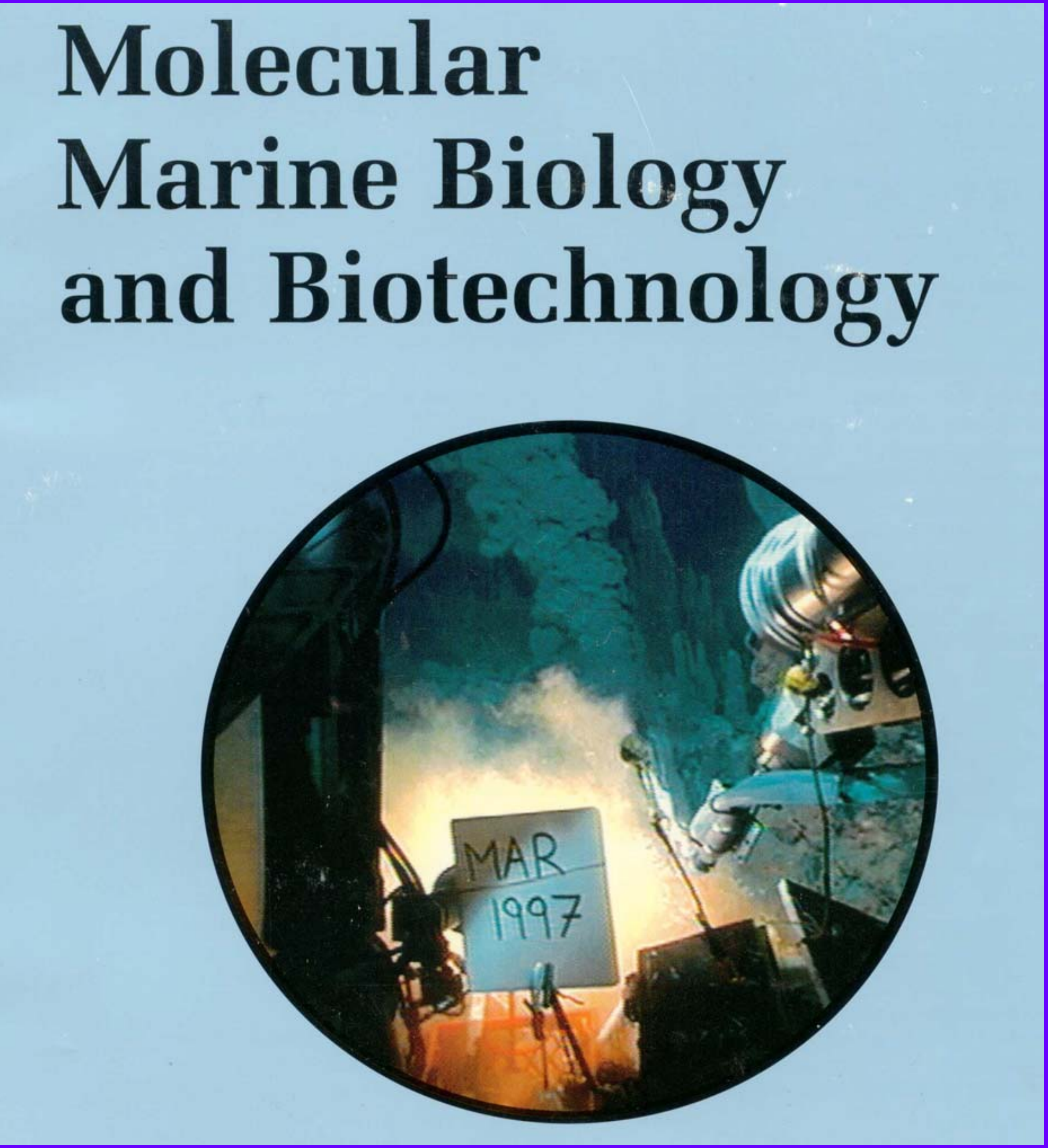


Cryptic species



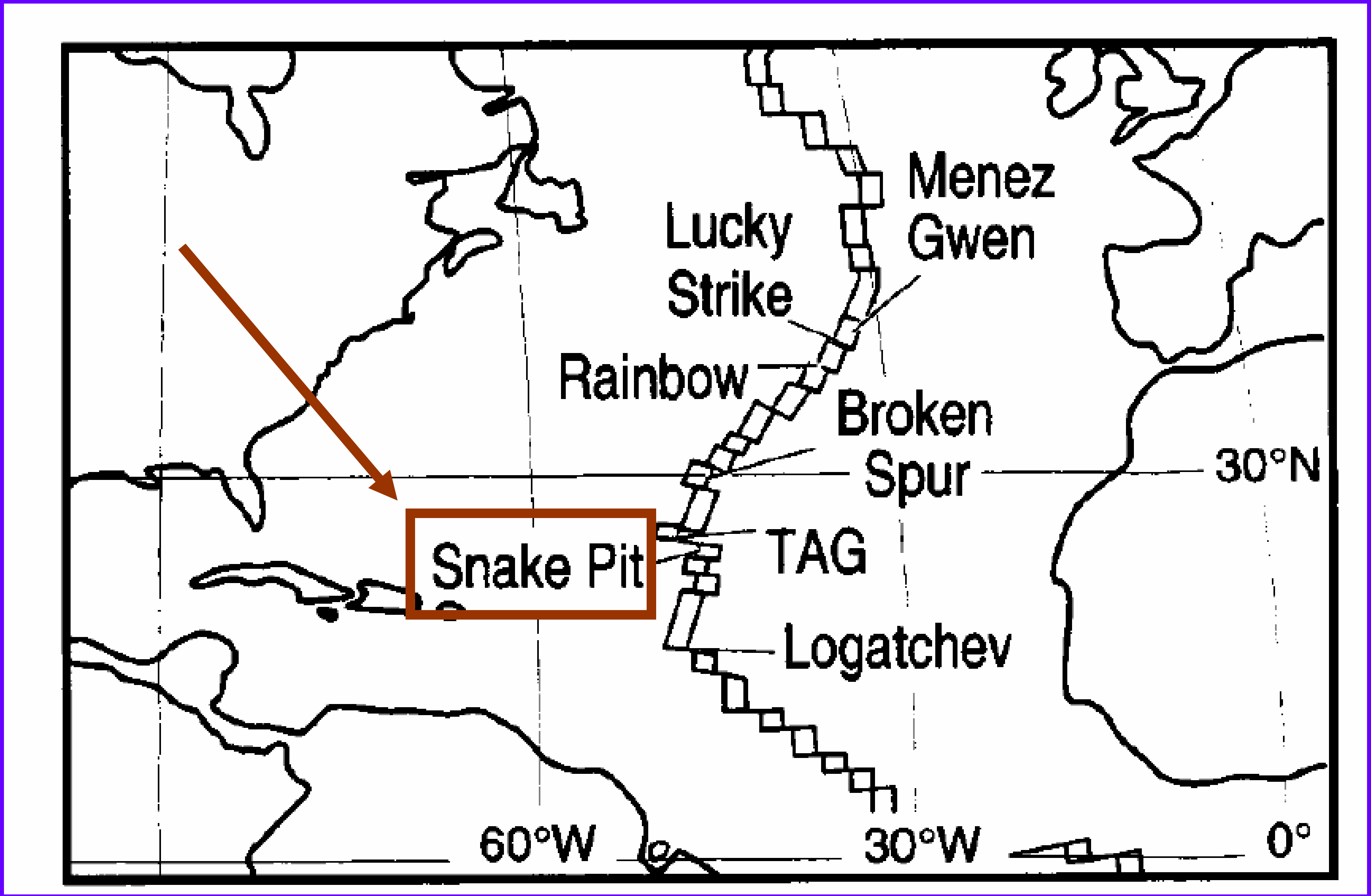


Colborn et al. 2001. The evolutionary enigma of bonefishes (*Albula* spp.): Cryptic species and ancient separations in a globally distributed shorefish. Evolution 55:807-820.

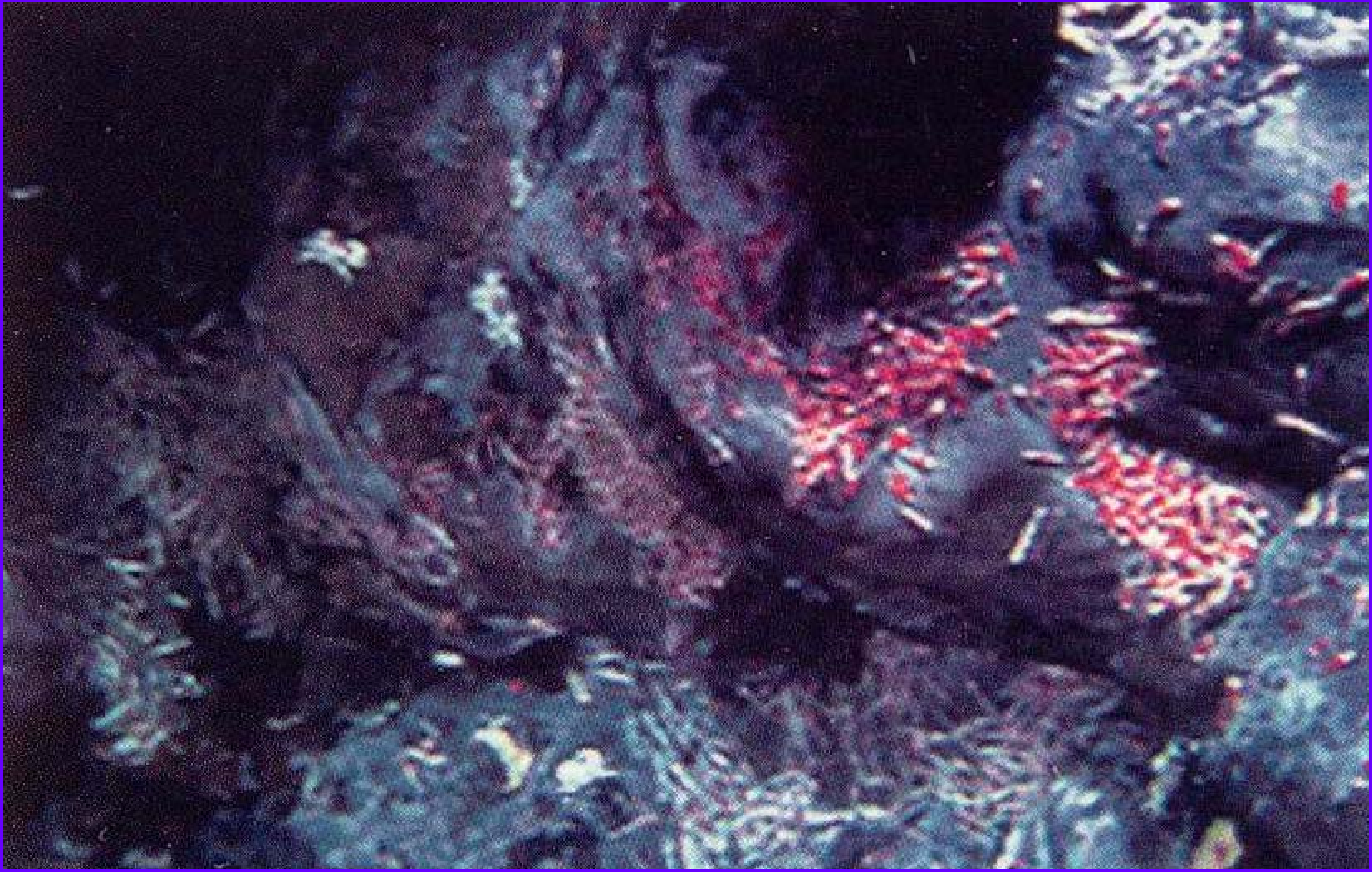


The mystery of the small orange shrimp

Mid-Atlantic Ridge system



Moose pit in Snake Pit hydrothermal vent area



Rimicaris exoculata

Iorania concordia (1996)

Rimicaris aurantiaca (1997)

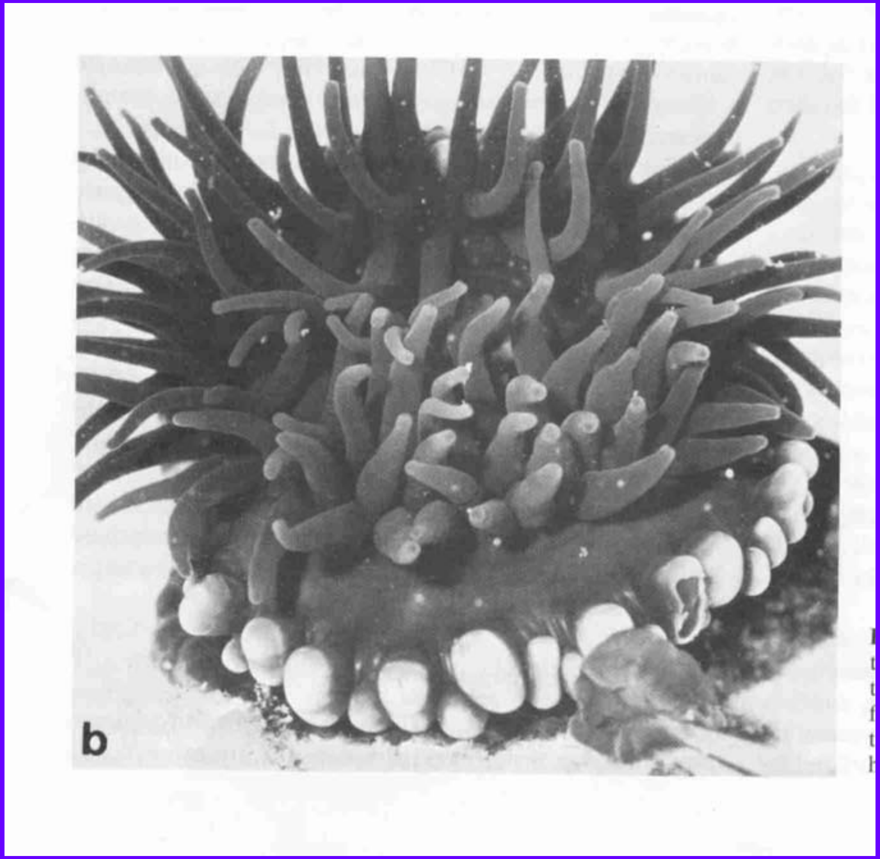
Rimicaris exoculata (1997)

Allozyme locus and shrimp form	Genotype frequencies		
	C/C	*C/R*	*R/R*
Pgm			
"Small orange"	24 (22.5)	4 (7.1)	1 (0.2)
R. exoculata	23 (22.5)	6 (6.9)	1 (0.4)
Pgi			
"Small orange"	9 (8.4)	14 (15.2)	7 (6.4)
R. exoculata	6 (6.4)	16 (15.2)	8 (8.4)
Gota			
"Small orange"	22 (22.5)	8 (7.1)	0 (0.4)
R. exoculata	25 (25.2)	5 (4.6)	0 (0.2)
Ap			
"Small orange"	27 (27.1)	3 (2.8)	0 (0.1)
R. exoculata	24 (22.5)	5 (7.1)	1 (0.4)

Small orange shrimp are juvenile *Rimicaris exoculata!*

9. Black and Johnson (1979) reported an highly unusual pattern of inheritance of allozyme polymorphisms in the intertidal anemone *Actina tenebrosa* from Rottnest Island in Western Australia. This species is viviparous, and up to 5 young are brooded by adults at a time until they are released as relatively large juveniles. The following parental and progeny genotypes were found at three allozyme loci:

Intertidal anemone



Asexual reproduction

Locus	Parental genotype	No. of broods	Progeny genotypes		
			FF	*FS*	*SS*
MDH	*FF*	25	68	0	0
	FS	53	0	158	0
	SS	11	0	0	35
PGM	*FF*	44	145	0	0
	FS	9	0	33	0
SOD	*FF*	71	225	0	0
	FS	18	0	50	0
	SS	1	0	0	2